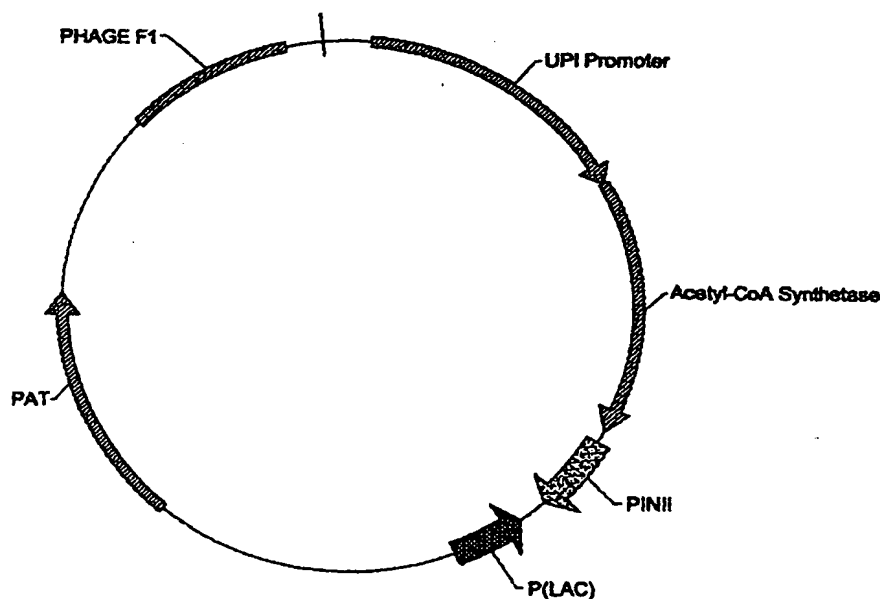




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(54) Title: COMPOSITIONS AND METHODS FOR ALTERING AN ACETYL-CoA METABOLIC PATHWAY OF A PLANT

**(57) Abstract**

Compositions and methods for altering the content of plant seeds are provided. The compositions comprise nucleotide sequences encoding the enzyme acetyl-CoA synthetase. Such compositions find use in increasing the biosynthesis of fatty acids and/or carotenoids in plants. By expressing the sequences utilizing seed-specific promoters, plant seed can be obtained having increased levels of oils, specialty oils, carotenoids, and amino acids.

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COMPOSITIONS AND METHODS FOR ALTERING AN ACETYL-CoA METABOLIC PATHWAY OF A PLANT

FIELD OF THE INVENTION

The invention relates to the genetic manipulation of plants, particularly to altering metabolic end products in plants and plant seeds.

5 BACKGROUND OF THE INVENTION

A long time goal of scientists has been to improve the fatty acid profile for oils. The oxidative stability of the vegetable oil is related to the number of double bonds in its fatty acids. That is, molecules with several double bonds are recognized to be more unstable. Thus, scientists have attempted to reduce the
10 amount of alpha-linolenic acid in order to improve shelf life and oxidative stability. Unfortunately, the use of naturally occurring germplasm has not proven to be successful by traditional breeding mechanisms.

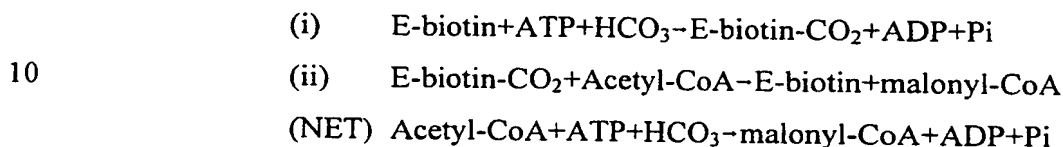
Other work has concentrated on producing modified oils with specific fatty acid composition, particularly very high oleic acid oils. High-oleic canola,
15 safflower, and sunflower oils as well as low-linolenic canola and soybean oils are on the market, although in limited quantities.

Modified oils are needed because of the stability as well as for health concerns. For example, high-oleic sunflower oil has about 1/3 the saturated fat content of cottonseed oil.

20 A major source of fatty acids is biosynthesis from small-molecule intermediates derived from metabolic breakdown of sugars, some amino acids, and other fatty acids. Acetyl-CoA is the direct source of all carbon atoms for the synthesis of palmitic acid. In a majority of instances the saturated straight-chain C16 acid, palmitic acid, is first synthesized and all other fatty acids are made by
25 modification of palmitic acid. Fatty acids are synthesized by sequential addition of 2-carbon units to the activated carboxyl end of a growing chain.

Acetyl-CoA Carboxylase (ACCase) catalyzes the formation of malonyl-CoA from acetyl-CoA and bicarbonate in animal, plant, and bacterial cells.

Malonyl-CoA is an essential substrate for (i) de novo fatty acid synthesis, (ii) fatty acid elongation, (iii) synthesis of secondary metabolites such as flavonoids and anthocyanins, and (iv) malonylation of some amino acids and secondary metabolites. Synthesis of malonyl-CoA is the first committed step of flavonoid and fatty acid synthesis and current evidence suggests that ACCase catalyzes the primary regulatory or rate-limiting step of fatty acid synthesis. Formation of malonyl-CoA by ACCase occurs via two partial reactions and requires a biotin prosthetic group:



In bacteria such as *Escherichia coli*, the ACCase has four distinct, separable protein subunit components; a biotin carboxyl carrier protein, a biotin carboxylase and two subunits of carboxyltransferase. In eukaryotes, ACCase is composed of multimers of a single multifunctional polypeptide having a molecular mass typically greater than 200 kDa (Samols *et al.*, *J. Biol. Chem.* 263:6461-6464 (1988)). These multimers have molecular masses ranging from 400 kDa to 8 MDa.

De novo fatty acid synthesis in chloroplasts involves successive 2-carbon additions to acetate, using malonate as the 2-C donor. All intermediates are attached to acyl carrier protein (ACP). Synthesis in plastids resembles that in *E. coli* in that the fatty acid synthesis complex can be dissociated into separate enzymes: β -ketoacyl-ACP synthase (KAS), β -ketoacyl-ACP reductase, β -hydroxyl-ACP dehydratase, and enoyl-ACP reductase, acetyl-CoA:ACP transacylase, and malonyl-CoA:ACP transacylase. A highly active KASIII isozyme catalyzes the condensation of acetyl-CoA and malonyl-ACP. Successive additions of malonyl-CoA to acyl-ACPs catalyzed by KASI form C16 acyl-ACP, some of which is converted to C18 acyl-ACP by KASII and then to C18:1-ACP. Fatty acid metabolism then diverges. De-esterification allows movement to the cytoplasm (eukaryotic path) where fatty acids may be further unsaturated and/or elongated by additions of malonyl-CoA in the ER. Alternatively, fatty acids are linked to glycerol-3 phosphate (prokaryotic path), further unsaturated, and used for synthesis of chloroplast lipids. A portion of cytoplasmic lipids returns to the chloroplast. The relative contributions of these two paths are species-specific but

appear to be relatively flexible in mutants blocked in either path. In oil-storing organs such as cotyledons and monocot embryos, the triacylglycerides are stored in cytoplasmic oil bodies surrounded by a single unit membrane.

5 Lipids, particularly triglycerides, have a great deal of commercial value in food and industrial products. Sunflower, safflower, rape, olive, soybean, peanut, flax, castor, oil palm, coconut and cotton are examples of major crops which are grown primarily or secondarily for their lipids. All agricultural animals provide animal sources for commercial fats and oils.

10 Seeds contain oil, starch, and protein in proportions which depend upon the plant species, cultivar and the stage of development. In the mature seed of oil seed rape, the main storage products are oil and protein, but starch accumulates transiently during the early phase of oil deposition. In non-photosynthetic tissues the synthesis of starch and fatty acids occurs in the plastids and requires the supply of carbon precursors from the cytosol.

15 There is needed a method for producing significant levels of fatty acids, carotenoids and other metabolic products in plants, particularly plant seeds. Such altered seeds would be useful nutritionally as well as provide a source for specialty oils and compounds.

20 SUMMARY OF THE INVENTION

Compositions and methods for modulating a metabolic pathway of a cell, particularly those pathways utilizing acetyl-CoA as a starting material, are provided. Such metabolic pathways include fatty acid biosynthesis, synthesis of isoprenoid compounds, and production of amino acids. The compositions
25 comprise nucleotide sequences encoding the enzyme acetyl-CoA synthetase (ACS). ACS catalyzes formation of acetyl-CoA. Acetyl-CoA is a precursor to fatty acids in plastids through a four-step process using the substrate acetate.

The compositions and methods find use in increasing biosynthesis of fatty acids and/or carotenoids in plants. Thus, utilizing the methods of the invention,
30 seed can be obtained having increased levels of oils, specialty oils, carotenoids, and amino acids genetically altering the content of seed. The methods involve preparing expression constructs with the nucleotide sequences of the invention and

the utilization of such constructs to prepare plants having altered metabolic pathways.

The nucleotide sequences of the invention can be used in combination with other genes and antisense sequences to alter the content of a plant seed. In this manner plant seeds having high oil content, specialty oils, increased essential amino acids, carotenoids and other metabolites can be obtained.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 provides a plasmid for the expression of acetyl-CoA synthetase using a ubiquitin promoter.

DETAILED DESCRIPTION OF THE INVENTION

In accordance with the subject invention, methods for modulating a metabolic pathway of a cell, particularly pathways utilizing acetyl-CoA as a substrate, hereinafter "acetyl-CoA pathways" are provided. Acetyl-CoA pathways are those pathways utilizing acetyl-CoA as a starting material and include fatty acid biosynthesis, isoprenoid biosynthesis, and production of amino acids. Thus, the methods of the invention provide for increasing and altering fatty acids, carotenoids, and/or amino acids in a plant, particularly plant seeds. The method involves transforming a plant with at least one gene encoding the enzyme acetyl-CoA synthetase (ACS). The plant may also comprise at least one additional gene, a second gene, that can be utilized to shunt the acetyl-CoA into the metabolic pathway of choice or to block a metabolic pathway for the production of other metabolites.

Compositions of the invention include two maize acetyl-CoA synthetase enzymes that are involved in catalyzing the formation of acetyl-CoA. In particular, the present invention provides for isolated nucleic acid molecules comprising nucleotide sequences encoding the amino acid sequences shown in SEQ ID NOS: 2 and 4. Further provided are polypeptides having an amino acid sequence encoded by a nucleic acid molecule described herein, for example those set forth in SEQ ID NOS: 1 and 3 and fragments and variants thereof.

The invention encompasses isolated or substantially purified nucleic acid or protein compositions. An "isolated" or "purified" nucleic acid molecule or protein,

or biologically active portion thereof, is substantially free of other cellular material, or culture medium when produced by recombinant techniques, or substantially free of chemical precursors or other chemicals when chemically synthesized.

Preferably, an "isolated" nucleic acid is free of sequences (preferably protein encoding sequences) that naturally flank the nucleic acid (i.e., sequences located at the 5' and 3' ends of the nucleic acid) in the genomic DNA of the organism from which the nucleic acid is derived. For example, in various embodiments, the isolated nucleic acid molecule can contain less than about 5 kb, 4 kb, 3 kb, 2 kb, 1 kb, 0.5 kb, or 0.1 kb of nucleotide sequences that naturally flank the nucleic acid molecule in genomic DNA of the cell from which the nucleic acid is derived. A protein that is substantially free of cellular material includes preparations of protein having less than about 30%, 20%, 10%, 5%, (by dry weight) of contaminating protein. When the protein of the invention or biologically active portion thereof is recombinantly produced, preferably culture medium represents less than about 30%, 20%, 10%, or 5% (by dry weight) of chemical precursors or non-protein-of-interest chemicals.

Acetyl-CoA synthetase is a key enzyme in plastids of higher plants which provides the starting substrate in acetyl-CoA for de novo fatty acid biosynthesis. ACS exhibits a high substrate specificity for acetate as compared to other organic acids. ACS plays a central role in several biosynthetic pathways. Besides de novo fatty acid biosynthesis, ACS is needed for the synthesis of mevalonic acid and isoprenoid lipids as well as branched-chain amino acids. Thus, it is recognized that the methods of the invention find use in altering a metabolite of interest in a plant, particularly in a plant seed. For purposes of the invention metabolites include fatty acids, carotenoids, and amino acids.

By increasing the biosynthesis of a metabolite is intended that the levels are increased over the levels in a native untransformed seed. That is, the levels are increased at least 2 fold to at least 10 fold in the transformed seed. In some instances significant increases of the metabolite can be obtained.

By "significant increase" is intended at least about a 10 to about a 50 fold increase, preferably at least about a 25 to about a 50 fold increase, more preferably about a 25 to about a 100 fold increase. Thus, the seed of the invention is a

significant source of the metabolite, fatty acid, carotenoid, or amino acids of interest.

The synthesis of acetyl-CoA, catalyzed by ACS is the first step in the synthesis of long-chain fatty acids from exogenous acetate by isolated, illuminated chloroplasts. Chloroplasts have been shown to be the sole repository of ACS in spinach cells. ACS activity has been detected in all chloroplast preparations so far examined and where comparison can be made, its activity normally exceeds that of pyruvate dehydrogenase by at least two-to five-fold. Additionally, in almost every case where comparisons have been made, acetate has been shown to be the preferred substrate for chloroplast fatty acid synthesis. The presence of acetate in incubations has strongly inhibited the incorporation of other precursors into fatty acids.

As acetyl-CoA in plant cells provides the starting substrate for key metabolic pathways, transformation of the plant cell with a nucleotide sequence encoding an acetyl-CoA synthetase results in increased metabolic activity. By transforming the plant with at least a second gene, the acetyl-CoA can be shunted into the particular metabolic pathway of choice. For example, for the production of fatty acids, the second gene may comprise nucleic acid sequence encoding acetyl-CoA carboxylase (ACCase). See, for example, WO 98/05758. Transformation with a second gene encoding an enzyme in the fatty acid pathway leads to a significant increase in the flux for the production of fatty acids. That is, there is an increase in the metabolic activity that can be further manipulated for the production of increased and/or altered fatty acid composition in the transformed seed.

To further increase the flux into fatty acid biosynthesis, an antisense construct for a nucleotide sequence encoding a protein in the carotenoid pathway can be utilized. Such nucleotide sequences include, IPP isomerase (Hahn *et al.* (1996) *J. Bacteriol.* 178:619-624 and the references cited therein, GenBank Accession Nos. U48963 and X82627, GenBank Accession No. U48962, GenBank Accession No. U48961, GenBank Accession No. X14230); geranylgeranyl pyrophosphate synthase (Misawa *et al.* (1990) *J. Bacteriol.* 172:6704-6712 and Application WO 91/13078); phytoene synthase (Misawa *et al.* (1990) *J. Bacteriol.* 172:6704-6712, GenBank Accession No. D90087, Application WO 91/13078,

- Armstrong *et al.* (1989) *Mol. Gen. Genet.* 216:254-268, Armstrong, G. A. "Genetic Analysis and Regulation of Carotenoid Biosynthesis." In R. C. Blankenship, M. T. Madigan, and C. E. Bauer (ed.), *Anoxygenic photosynthetic bacteria; advances in photosynthesis*. Kluwer Academic Publishers, Dordrecht, The Netherlands,
- 5 Armstrong *et al.* (1990) *Proc. Natl. Acad. Sci. USA* 87:9975-9979, Armstrong *et al.* (1993) *Methods Enzymol.* 214:297-311, Bartley and Scolnik (1993) *J. Biol. Chem.* 268:27518-27521, Bartley *et al.* (1992) *J. Biol. chem.* 267:5036-5039, Bramley *et al.* (1992) *Plant J.* 2:291-343, Ray *et al.* (1992) *Plant Mol. Biol.* 19:401-404, Ray *et al.* (1987) *Nucleic Acids Res.* 15:10587, Romer *et al.* (1994) *Biochem.*
- 10 *Biophys. Res. Commun.* 196:1414-1421, Karvouni *et al.* (1995) *Plant Molecular Biology* 27:1153-1162, GenBank Accession Nos. U32636, Z37543, L37405, X95596, D58420, U32636, Z37543, X78814, X82458, S71770, L27652, L23424, X68017, L25812, M87280, M38424, X69172, X63873, and X60441, Armstrong, G. A. (1994) *J. Bacteriol.* 176:4795-4802 and the references cited therein); and,
- 15 phytoene desaturase (Misawa *et al.* (1990) *J. Bacteriol.* 172:6704-6712, Application WO 91/13078, GenBank Accession Nos. L37405, X95596, D58420, X82458, S71770, and M87280). See, also, Misawa *et al.* (1990) *J. of Bacteriology* 172:6704-6712, E. P. 0393690 B1, U.S. Patent No. 5,429,939, Bartley *et al.* (1992) *J. Biol. Chem.* 267:5036-5039, Bird *et al.* (1991) *Biotechnology* 9:635-639, and U.
- 20 S. Patent No. 5,304,478, which disclosures are herein incorporated by reference.

Once the pathway for fatty acid biosynthesis has been primed, additional coding sequences in the fatty acid biosynthesis pathway and corresponding antisense sequences can be used for the production of a high concentration of specialty oils. See, for example, Poulouse *et al.* (1985) *J. Biol. Chem.* 260:15953-

25 15958 (S-acyl fatty acid synthase); Bayley *et al.* (1988) *BioTechnology* 6:1219-1221 (medium chain hydrolase gene); Mizamoto *et al.* (1988) *J. Biol. Chem.* 265:13393-13399 (fatty acid reductase); Naggert *et al.* (1987) *Biochem. J.* 243:597-601 (S-acyl fatty acid synthase thioester hydrolase); Smith *et al.* (1986) *Biochem. Soc. Trans.* 14:583-584 (acyl-ACP thioesterase II); 5,559,220 (acetyl

30 Coenzyme A carboxylase); WO98/05758 (acetyl-CoA carboxylase); and the like. See also, U.S. Patent Nos. 5,411,879; 5,455,167; 5,512,482; 5,344,771; and 5,679,881. Such disclosures are herein incorporated by reference.

For the production of carotenoids, the second gene may correspond to a coding sequence for an enzyme in the carotenoid pathway. Such second genes may be utilized to shunt the acetyl-CoA into carotenoid biosynthesis. In this manner, an increase in the biosynthetic activity of the carotenoid pathway is seen, and increased production of particular carotenoids such as α - and β -carotene can be produced. As with the production of specialty fatty acids, once the biosynthetic activity has been increased, the pathway can be diverted for the production of specific compounds by using any of the coding sequences or antisense constructs for carotenoid biosynthesis. See, above. This diversion may involve the action of at least a third gene of interest. The third gene encodes an enzyme to force the production of a particular compound or alternatively, can encode a protein to stop the pathway for the accumulation of a particular compound.

To stop the pathway, an antisense RNA can be utilized for the accumulation of a particular compound. Alternatively, homologous plant sequences or partial plant sequences can be used to stop the pathway. For example, for the production of lycopene, an antisense lycopene ϵ -cyclase and the coding sequence for lycopene β -cyclase (Hugueney *et al.* (1995) *Plant J.* 8:417-424, Cunningham *et al.* (1994) *Plant Cell* 6:1107-1121, Scholnik and Bartley (1995) *Plant Physiol.* 108:1343) are utilized.

In this manner, the metabolic pathway of interest can be manipulated for the high production of any particular compound of interest in the pathway. Likewise, the pathway can be manipulated to decrease levels of a particular compound by transformation of antisense DNA sequences that prevent the conversion of the precursor compound into the particular compound being regulated. In the same manner, to increase the biosynthesis of branched-chain amino acids, antisense constructs for fatty acid biosynthesis and carotenoid biosynthesis can be utilized. In this embodiment, the acetyl-CoA is shunted into the production of amino acids or secondary metabolites of interest.

Any means for producing a plant comprising the acetyl-CoA synthetase coding sequence or both the acetyl-CoA synthetase and at least a second gene are encompassed by the present invention. For example, the second (or additional) gene of interest can be used to transform a plant at the same time as the acetyl-CoA synthetase (cotransformation), the second gene can be introduced into a plant that

has already been transformed with the acetyl-CoA synthetase, or alternatively, transformed plants, one expressing the acetyl-CoA synthetase and one expressing the second gene, can be crossed to bring the genes together in the same plant.

Subsequent crosses or transformations can bring additional sequences together in the plant.

By combining the genes with tissue-specific promoters, the metabolite of interest can be altered in particular tissues of the plant. Thus, fatty acid or carotenoid levels in the seed, including embryos and endosperm, can be altered by the use of seed-specific promoters or transcription initiation regions. In addition, other promoters associated with storage proteins or involved in fatty acid biosynthesis may be used.

"Seed-preferred" promoters include both "seed-specific" promoters (those promoters active during seed development such as promoters of seed storage proteins) as well as "seed-germinating" promoters (those promoters active during seed germination). See Thompson *et al.* (1989) *BioEssays* 10:108, herein incorporated by reference. Such seed-preferred promoters include, but are not limited to, Cim1 (cytokinin-induced message); cZ19B1 (maize 19 kDa zein); milps (myo-inositol-1-phosphate synthase); EA9; acyl carrier protein; and celA (cellulose synthase) (see the copending application entitled "Seed-Preferred Promoters," U.S. Patent Application Serial No. 60/097,233, filed August 20, 1998, herein incorporated by reference). Gama-zein is a preferred endosperm-specific promoter. Glob-1 is a preferred embryo-specific promoter. For dicots, seed-specific promoters include, but are not limited to, bean β -phaseolin, napin, β -conglycinin, soybean lectin, cruciferin, and the like. For monocots, seed-specific promoters include, but are not limited to, maize 15 kDa zein, 22 kDa zein, 27 kDa zein, g-zein, waxy, shrunken 1, shrunken 2, globulin 1, etc.

Nucleic acid sequences encoding acetyl-CoA synthetase have been isolated from other organisms. It is recognized that other known acetyl-CoA synthetase sequences may be used in the methods of the invention and include, but are not limited to, those described in Shin *et al.* (1977) *FEMS Microbiol. Lett.* 146:103-108; Garre *et al.* (1994) *Mol. Gen. Genet.* 244:278-286; and De Virgilio *et al.* (1992) *Yeast* 8:1043-1051.

The maize sequences can be used to isolate other nucleic acid sequences encoding acetyl-CoA synthetase from other plants. The entire nucleotide sequences as well as fragments or variants thereof may be used in the method of the invention.

5 Fragments and variants of the disclosed nucleotide sequences and proteins encoded thereby are also encompassed by the present invention. By "fragment" is intended a portion of the nucleotide sequence or a portion of the amino acid sequence and hence protein encoded thereby. Fragments of a nucleotide sequence may encode protein fragments that retain the biological activity of the native
10 protein and hence catalyzes the formation of acetyl-CoA. Alternatively, fragments of a nucleotide sequence that are useful as hybridization probes generally do not encode fragment proteins retaining biological activity. Thus, fragments of a nucleotide sequence may range from at least about 20 nucleotides, about 50 nucleotides, about 100 nucleotides, and up to the full-length nucleotide sequence
15 encoding the proteins of the invention.

A fragment of an acetyl-CoA synthetase nucleotide sequence that encodes a biologically active portion of an acetyl-CoA synthetase protein of the invention will encode at least 20, 25, 30, 50, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600 contiguous amino acids, or up to the total number of amino acids present
20 in a full-length acetyl-CoA synthetase protein of the invention (for example, 632 amino acids for both SEQ ID NOS: 2 and 4). Fragments of an acetyl-CoA synthetase nucleotide sequence that are useful as hybridization probes for PCR primers generally need not encode a biologically active portion of an acetyl-CoA synthetase protein.

25 Thus, a fragment of an acetyl-CoA synthetase nucleotide sequence may encode a biologically active portion of an acetyl-CoA synthetase protein, or it may be a fragment that can be used as a hybridization probe or PCR primer using methods disclosed below. A biologically active portion of an acetyl-CoA synthetase protein can be prepared by isolating a portion of one of the acetyl-CoA
30 synthetase nucleotide sequences of the invention, expressing the encoded portion of the acetyl-CoA synthetase protein (e.g., by recombinant expression *in vitro*), and assessing the activity of the encoded portion of the acetyl-CoA synthetase protein. Nucleic acid molecules that are fragments of an acetyl-CoA synthetase nucleotide

sequence comprise at least 16, 20, 50, 75, 100, 150, 200, 250, 300, 350, 400, 500, 600, 700, 800, 900, 1,000, 1,100, 1,200, 1,300, 1,400, 1,500, 1,600, 1,700, 1,800, 1,900, 2,000 nucleotides, or up to the number of nucleotides present in a full-length acetyl-CoA synthetase nucleotide sequence disclosed herein (for example, 2,007 and 2,005 nucleotides for SEQ ID NOS: 1 and 3, respectively).

By "variants" is intended substantially similar sequences. For nucleotide sequences, conservative variants include those sequences that, because of the degeneracy of the genetic code, encode the amino acid sequence of one of the acetyl-CoA synthetase polypeptides of the invention. Naturally occurring variants such as these can be identified with the use of well-known molecular biology techniques, as, for example, with polymerase chain reaction (PCR) and hybridization techniques as outlined below. Variant nucleotide sequences also include synthetically derived nucleotide sequences, such as those generated, for example, by using site-directed mutagenesis but which still encode a acetyl-CoA synthetase protein of the invention. Generally, nucleotide sequence variants of the invention will have at least 40%, 50%, 60%, 70%, generally, 80%, preferably 85%, 90%, up to 95%, 98% sequence identity to its respective native nucleotide sequence.

By "variant" protein is intended a protein derived from the native protein by deletion (so-called truncation) or addition of one or more amino acids to the N-terminal and/or C-terminal end of the native protein; deletion or addition of one or more amino acids at one or more sites in the native protein; or substitution of one or more amino acids at one or more sites in the native protein. Such variants may result from, for example, genetic polymorphism or from human manipulation.

The proteins of the invention may be altered in various ways including amino acid substitutions, deletions, truncations, and insertions. Methods for such manipulations are generally known in the art. For example, amino acid sequence variants of the acetyl-CoA synthetase proteins can be prepared by mutations in the DNA. Methods for mutagenesis and nucleotide sequence alterations are well known in the art. See, for example, Kunkel (1985) *Proc. Natl. Acad. Sci. USA* 82:488-492; Kunkel *et al.* (1987) *Methods in Enzymol.* 154:367-382; US Patent No. 4,873,192; Walker and Gaastra, eds. (1983) *Techniques in Molecular Biology* (MacMillan Publishing Company, New York) and the references cited therein.

Guidance as to appropriate amino acid substitutions that do not affect biological activity of the protein of interest may be found in the model of Dayhoff *et al.* (1978) *Atlas of Protein Sequence and Structure* (Natl. Biomed. Res. Found., Washington, D.C.), herein incorporated by reference. Conservative substitutions, such as exchanging one amino acid with another having similar properties, may be preferred.

Thus, the genes and nucleotide sequences of the invention include both the naturally occurring sequences as well as mutant forms. Likewise, the proteins of the invention encompass both naturally occurring proteins as well as variations and modified forms thereof. Such variants will continue to possess the desired ability to catalyze the formation of acetyl-CoA. Obviously, the mutations that will be made in the DNA encoding the variant must not place the sequence out of reading frame and preferably will not create complementary regions that could produce secondary mRNA structure. See, EP Patent Application Publication No. 75,444.

The deletions, insertions, and substitutions of the protein sequences encompassed herein are not expected to produce radical changes in the characteristics of the protein. However, when it is difficult to predict the exact effect of the substitution, deletion, or insertion in advance of doing so, one skilled in the art will appreciate that the effect will be evaluated by routine screening assays. That is, the activity can be evaluated by assaying for the altered biosynthesis of a metabolite of interest.

Variant nucleotide sequences and proteins also encompass sequences and proteins derived from a mutagenic and recombinogenic procedure such as DNA shuffling. With such a procedure, one or more different acetyl-CoA synthetase coding sequences can be manipulated to create a new acetyl-CoA synthetase possessing the desired properties. In this manner, libraries of recombinant polynucleotides are generated from a population of related sequence polynucleotides comprising sequence regions that have substantial sequence identity and can be homologously recombined *in vitro* or *in vivo*. For example, using this approach, sequence motifs encoding a domain of interest may be shuffled between the acetyl-CoA synthetase nucleic acid sequence of the invention and other known acetyl-CoA synthetase nucleotide sequences to obtain a new gene coding for a protein with an improved property of interest, such as an increased K_m

in the case of an enzyme. Strategies for such DNA shuffling are known in the art. See, for example, Stemmer (1994) *Proc. Natl. Acad. Sci. USA* 91:10747-10751; Stemmer (1994) *Nature* 370:389-391; Crameri *et al.* (1997) *Nature Biotech.* 15:436-438; Moore *et al.* (1997) *J. Mol. Biol.* 272:336-347; Zhang *et al.* (1997) *Proc. Natl. Acad. Sci. USA* 94:4504-4509; Crameri *et al.* (1998) *Nature* 391:288-291; and U.S. Patent Nos. 5,605,793 and 5,837,458.

The nucleotide sequences of the invention can be used to isolate corresponding sequences from other organisms, particularly other plants, and more particularly other monocots. In this manner, methods such as PCR, hybridization, and the like can be used to identify such sequences based on their sequence homology to the sequences set forth herein. Sequences isolated based on their sequence identity to the entire sequences set forth herein or to fragments thereof are encompassed by the present invention.

In a PCR approach, oligonucleotide primers can be designed for use in PCR reactions to amplify corresponding DNA sequences from cDNA or genomic DNA extracted from any plant of interest. Methods for designing PCR primers and PCR cloning are generally known in the art and are disclosed in Sambrook *et al.* (1989) *Molecular Cloning: A Laboratory Manual* (2d ed., Cold Spring Harbor Laboratory Press, Plainview, New York). See also Innis *et al.*, eds. (1990) *PCR Protocols: A Guide to Methods and Applications* (Academic Press, New York); Innis and Gelfand, eds. (1995) *PCR Strategies* (Academic Press, New York); and Innis and Gelfand, eds. (1999) *PCR Methods Manual* (Academic Press, New York). Known methods of PCR include, but are not limited to, methods using paired primers, nested primers, single specific primers, degenerate primers, gene-specific primers, vector-specific primers, partially-mismatched primers, and the like.

In hybridization techniques, all or part of a known nucleotide sequence is used as a probe that selectively hybridizes to other corresponding nucleotide sequences present in a population of cloned genomic DNA fragments or cDNA fragments (*i.e.*, genomic or cDNA libraries) from a chosen organism. The hybridization probes may be genomic DNA fragments, cDNA fragments, RNA fragments, or other oligonucleotides, and may be labeled with a detectable group such as ^{32}P , or any other detectable marker. Thus, for example, probes for hybridization can be made by labeling synthetic oligonucleotides based on the

acetyl-CoA synthetase sequences of the invention. Methods for preparation of probes for hybridization and for construction of cDNA and genomic libraries are generally known in the art and are disclosed in Sambrook *et al.* (1989) *Molecular Cloning: A Laboratory Manual* (2d ed., Cold Spring Harbor Laboratory Press, Plainview, New York).

For example, the entire acetyl-CoA synthetase sequence disclosed herein, or one or more portions thereof, may be used as a probe capable of specifically hybridizing to corresponding acetyl-CoA synthetase sequences and messenger RNAs. To achieve specific hybridization under a variety of conditions, such probes include sequences that are unique among acetyl-CoA synthetase sequences and are preferably at least about 10 nucleotides in length, and most preferably at least about 20 nucleotides in length. Such probes may be used to amplify corresponding acetyl-CoA synthetase sequences from a chosen plant by PCR. This technique may be used to isolate additional coding sequences from a desired plant or as a diagnostic assay to determine the presence of coding sequences in a plant. Hybridization techniques include hybridization screening of plated DNA libraries (either plaques or colonies; see, for example, Sambrook *et al.* (1989) *Molecular Cloning: A Laboratory Manual* (2d ed., Cold Spring Harbor Laboratory Press, Plainview, New York).

Hybridization of such sequences may be carried out under stringent conditions. By "stringent conditions" or "stringent hybridization conditions" is intended conditions under which a probe will hybridize to its target sequence to a detectably greater degree than to other sequences (e.g., at least 2-fold over background). Stringent conditions are sequence-dependent and will be different in different circumstances. By controlling the stringency of the hybridization and/or washing conditions, target sequences that are 100% complementary to the probe can be identified (homologous probing). Alternatively, stringency conditions can be adjusted to allow some mismatching in sequences so that lower degrees of similarity are detected (heterologous probing). Generally, a probe is less than about 1000 nucleotides in length, preferably less than 500 nucleotides in length.

Typically, stringent conditions will be those in which the salt concentration is less than about 1.5 M Na ion, typically about 0.01 to 1.0 M Na ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30°C for short

probes (e.g., 10 to 50 nucleotides) and at least about 60°C for long probes (e.g., greater than 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. Exemplary low stringency conditions include hybridization with a buffer solution of 30 to 35% formamide, 1 M NaCl, 1% SDS (sodium dodecyl sulphate) at 37°C, and a wash in 1X to 2X SSC (20X SSC = 3.0 M NaCl/0.3 M trisodium citrate) at 50 to 55°C. Exemplary moderate stringency conditions include hybridization in 40 to 45% formamide, 1.0 M NaCl, 1% SDS at 37°C, and a wash in 0.5X to 1X SSC at 55 to 60°C. Exemplary high stringency conditions include hybridization in 50% formamide, 1 M NaCl, 1% SDS at 37°C, and a wash in 0.1X SSC at 60 to 65°C.

Specificity is typically the function of post-hybridization washes, the critical factors being the ionic strength and temperature of the final wash solution. For DNA-DNA hybrids, the T_m can be approximated from the equation of Meinkoth and Wahl (1984) *Anal. Biochem.* 138:267-284: $T_m = 81.5^\circ\text{C} + 16.6 (\log M) + 0.41 (\%GC) - 0.61 (\% \text{ form}) - 500/L$; where M is the molarity of monovalent cations, %GC is the percentage of guanosine and cytosine nucleotides in the DNA, % form is the percentage of formamide in the hybridization solution, and L is the length of the hybrid in base pairs. The T_m is the temperature (under defined ionic strength and pH) at which 50% of a complementary target sequence hybridizes to a perfectly matched probe. T_m is reduced by about 1°C for each 1% of mismatching; thus, T_m , hybridization, and/or wash conditions can be adjusted to hybridize to sequences of the desired identity. For example, if sequences with $\geq 90\%$ identity are sought, the T_m can be decreased 10°C. Generally, stringent conditions are selected to be about 5°C lower than the thermal melting point (T_m) for the specific sequence and its complement at a defined ionic strength and pH. However, severely stringent conditions can utilize a hybridization and/or wash at 1, 2, 3, or 4°C lower than the thermal melting point (T_m); moderately stringent conditions can utilize a hybridization and/or wash at 6, 7, 8, 9, or 10°C lower than the thermal melting point (T_m); low stringency conditions can utilize a hybridization and/or wash at 11, 12, 13, 14, 15, or 20°C lower than the thermal melting point (T_m). Using the equation, hybridization and wash compositions, and desired T_m , those of ordinary skill will understand that variations in the stringency of hybridization and/or wash solutions are inherently described. If the desired

degree of mismatching results in a T_m of less than 45°C (aqueous solution) or 32°C (formamide solution), it is preferred to increase the SSC concentration so that a higher temperature can be used. An extensive guide to the hybridization of nucleic acids is found in Tijssen (1993) *Laboratory Techniques in Biochemistry and Molecular Biology—Hybridization with Nucleic Acid Probes*, Part I, Chapter 2 (Elsevier, New York); and Ausubel *et al.*, eds. (1995) *Current Protocols in Molecular Biology*, Chapter 2 (Greene Publishing and Wiley-Interscience, New York). See Sambrook *et al.* (1989) *Molecular Cloning: A Laboratory Manual* (2d ed., Cold Spring Harbor Laboratory Press, Plainview, New York).

10 In general, sequences that encode for a acetyl-CoA synthetase protein and hybridize to the acetyl-CoA synthetase sequences disclosed herein will be at least 40% to 50% homologous, about 60% to 70% homologous, and even about 80%, 85%, 90%, 95% to 98% homologous or more with the disclosed sequences. That is, the sequence similarity of sequences may range, sharing at least about 40% to 15 50%, about 60% to 70%, and even about 80%, 85%, 90%, 95% to 98% sequence similarity.

The following terms are used to describe the sequence relationships between two or more nucleic acids or polynucleotides: (a) "reference sequence", (b) "comparison window", (c) "sequence identity", (d) "percentage of sequence 20 identity", and (e) "substantial identity".

(a) As used herein, "reference sequence" is a defined sequence used as a basis for sequence comparison. A reference sequence may be a subset or the entirety of a specified sequence; for example, as a segment of a full-length cDNA or gene sequence, or the complete cDNA or gene sequence.

25 (b) As used herein, "comparison window" makes reference to a contiguous and specified segment of a polynucleotide sequence, wherein the polynucleotide sequence in the comparison window may comprise additions or deletions (i.e., gaps) compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. Generally, the 30 comparison window is at least 20 contiguous nucleotides in length, and optionally can be 30, 40, 50, 100, or longer. Those of skill in the art understand that to avoid a high similarity to a reference sequence due to inclusion of gaps in the

polynucleotide sequence a gap penalty is typically introduced and is subtracted from the number of matches.

Methods of alignment of sequences for comparison are well known in the art. Optimal alignment of sequences for comparison may be conducted by the
5 local homology algorithm of Smith *et al.* (1981) *Adv. Appl. Math.* 2:482; by the homology alignment algorithm of Needleman *et al.* (1970) *J. Mol. Biol.* 48:443; by the search for similarity method of Pearson *et al.* (1988) *Proc. Natl. Acad. Sci.* 85:2444; by computerized implementations of these algorithms, including, but not limited to: CLUSTAL in the PC/Gene program by Intelligenetics, Mountain View,
10 California; GAP, BESTFIT, BLAST, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group (GCG), 575 Science Drive, Madison, Wisconsin, USA; the CLUSTAL program is well described by Higgins *et al.* (1988) *Gene* 73:237-244 (1988); Higgins *et al.* (1989) *CABIOS* 5:151-153; Corpet *et al.* (1988) *Nucleic Acids Res.* 16:10881-90; Huang *et al.* (1992)
15 *Computer Applications in the Biosciences* 8:155-65, and Person *et al.* (1994) *Meth. Mol. Biol.* 24:307-331; preferred computer alignment methods also include the BLASTP, BLASTN, and BLASTX algorithms (see Altschul *et al.* (1990) *J. Mol. Biol.* 215:403-410). Alignment is also often performed by inspection and manual alignment. The alignments are performed using the default parameters of the
20 sequence alignment programs.

(c) As used herein, "sequence identity" or "identity" in the context of two nucleic acid or polypeptide sequences makes reference to the residues in the two sequences that are the same when aligned for maximum correspondence over a specified comparison window. When percentage of sequence identity is used in
25 reference to proteins it is recognized that residue positions which are not identical often differ by conservative amino acid substitutions, where amino acid residues are substituted for other amino acid residues with similar chemical properties (e.g., charge or hydrophobicity) and therefore do not change the functional properties of the molecule. When sequences differ in conservative substitutions, the percent
30 sequence identity may be adjusted upwards to correct for the conservative nature of the substitution. Sequences that differ by such conservative substitutions are said to have "sequence similarity" or "similarity". Means for making this adjustment are well known to those of skill in the art. Typically this involves

scoring a conservative substitution as a partial rather than a full mismatch, thereby increasing the percentage sequence identity. Thus, for example, where an identical amino acid is given a score of 1 and a non-conservative substitution is given a score of zero, a conservative substitution is given a score between zero and 1. The
5 scoring of conservative substitutions is calculated, e.g., as implemented in the program PC/GENE (Intelligenetics, Mountain View, California).

(d) As used herein, "percentage of sequence identity" means the value determined by comparing two optimally aligned sequences over a comparison window, wherein the portion of the polynucleotide sequence in the comparison
10 window may comprise additions or deletions (i.e., gaps) as compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid base or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the
15 number of matched positions by the total number of positions in the window of comparison, and multiplying the result by 100 to yield the percentage of sequence identity.

(e)(i) The term "substantial identity" of polynucleotide sequences means that a polynucleotide comprises a sequence that has at least 70% sequence identity, preferably at least 80%, more preferably at least 90%, and most preferably at least
20 95%, compared to a reference sequence using one of the alignment programs described using standard parameters. One of skill in the art will recognize that these values can be appropriately adjusted to determine corresponding identity of proteins encoded by two nucleotide sequences by taking into account codon
25 degeneracy, amino acid similarity, reading frame positioning, and the like. Substantial identity of amino acid sequences for these purposes normally means sequence identity of at least 60%, more preferably at least 70%, 80%, 90%, and most preferably at least 95%.

Another indication that nucleotide sequences are substantially identical is if
30 two molecules hybridize to each other under stringent conditions. Generally, stringent conditions are selected to be about 5°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH. However, stringent conditions encompass temperatures in the range of about 1°C to about

20°C, depending upon the desired degree of stringency as otherwise qualified herein. Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the polypeptides they encode are substantially identical. This may occur, e.g., when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code. One indication that two nucleic acid sequences are substantially identical is when the polypeptide encoded by the first nucleic acid is immunologically cross reactive with the polypeptide encoded by the second nucleic acid.

- (e)(ii) The term "substantial identity" in the context of a peptide indicates that a peptide comprises a sequence with at least 70% sequence identity to a reference sequence, preferably 80%, more preferably 85%, most preferably at least 90% or 95% sequence identity to the reference sequence over a specified comparison window. Preferably, optimal alignment is conducted using the homology alignment algorithm of Needleman *et al.* (1970) *J. Mol. Biol.* 48:443. An indication that two peptide sequences are substantially identical is that one peptide is immunologically reactive with antibodies raised against the second peptide. Thus, a peptide is substantially identical to a second peptide, for example, where the two peptides differ only by a conservative substitution. Peptides that are "substantially similar" share sequences as noted above except that residue positions that are not identical may differ by conservative amino acid changes.

For the most part, the nucleotide sequences of interest of the present invention will be targeted to the chloroplast for expression to prevent systemic expression of the nucleic acid sequence which could result in morphological deformities. In this manner, where the gene of interest is not directly inserted into the chloroplast, the expression cassette will additionally contain a nucleic acid encoding a transit peptide to direct the gene of interest to the chloroplasts. Such transit peptides are known in the art. See, for example, Von Heijne *et al.* (1991) *Plant Mol. Biol. Rep.* 9:104-126; Clark *et al.* (1989) *J. Biol. Chem.* 264:17544-17550; della-Cioppa *et al.* (1987) *Plant Physiol.* 84:965-968; Romer *et al.* (1993) *Biochem. Biophys. Res Commun.* 196:1414-1421; and, Shah *et al.* (1986) *Science* 233:478-481. Plant carotenoid and fatty acid biosynthesis genes useful in the invention may utilize native or heterologous transit peptides.

Chloroplast targeting sequences are known in the art and include the chloroplast small subunit of ribulose-1,5-bisphosphate carboxylase (Rubisco), (de Castro Silva Filho *et al.* (1996) *Plant Mol. Biol.* 30:769-780; Schnell, *et al.* (1991) *J. Biol. Chem.* 266(5):3335-3342); 5-(enolpyruvyl)shikimate-3-phosphate synthase (EPSPS) (Archer *et al.* (1990) *J. Bioenerg. Biomemb.* 22(6):789-810); tryptophan synthase (Zhao *et al.* (1995) *J. Biol. Chem.* 270(11):6081-6087); plastocyanin (Lawrence *et al.* (1997) *J. Biol. Chem.* 272(33):20357-20363); chorismate synthase (Schmidt *et al.* (1993) *J. Biol. Chem.* 268(36):27477-27457); and the light harvesting chlorophyll a/b binding protein (LHBP) (Lamppa *et al.* (1988) *J. Biol. Chem.* 263:14996-14999). See also Von Heijne *et al.* (1991) *Plant Mol. Biol. Rep.* 9:104-126; Clark *et al.* (1989) *J. Biol. Chem.* 264:17544-17550; della-Cioppa *et al.* (1987) *Plant Physiol.* 84:965-968; Romer *et al.* (1993) *Biochem. Biophys. Res Commun.* 196:1414-1421; and Shah *et al.* (1986) *Science* 233:478-481.

Methods for transformation of chloroplasts are known in the art. See, for example, Svab *et al.* (1990) *Proc. Natl. Acad. Sci. USA* 87:8526-8530; Svab and Maliga (1993) *Proc. Natl. Acad. Sci. USA* 90:913-917; Staub and Maliga (1993) *Embo J.* 12:601-606. The method relies on particle gun delivery of DNA containing a selectable marker and targeting of the DNA to the plastid genome through homologous recombination. Additionally, plastid transformation can be accomplished by transactivation of a silent plastid-borne transgene by tissue-specific expression of a nuclear-encoded and plastid-directed RNA polymerase. Such a system has been reported in McBride *et al.* (1994) *Proc. Natl. Acad. Sci. USA* 91:7301-7305.

The sequences of the invention can be introduced into any plant. The sequences to be introduced may be used in expression cassettes for expression in any plant of interest where expression in the plant is necessary for transcription.

Of particular interest are plants where the seed is produced in high amounts, or the seed or a seed part is edible. Seeds of interest include the oil seeds, such as seeds from *Brassica*, cotton, soybean, safflower, sunflower, coconut, palm, etc.; grain seeds such as wheat, barley, rice, corn, etc.; other seeds including oats, pumpkin, squash, poppy, sesame, peanut, peas, beans, cocoa, coffee, etc.; and tree nuts such as walnuts, pecans, almonds, etc.

"Operably linked" includes reference to a functional linkage between a promoter and a second sequence, wherein the promoter sequence initiates and mediates transcription of the DNA sequence corresponding to the second sequence. Generally, operably linked means that the nucleic acid sequences being linked are
5 contiguous and, where necessary to join two protein coding regions, contiguous and in the same reading frame.

Nucleotide sequences of the invention are provided in expression cassettes for expression in the plant of interest. The cassette will include 5' and 3' regulatory sequences operably linked to the sequence of interest. The cassette may
10 additionally contain at least one additional sequence to be cotransformed into the organism. Alternatively, the additional sequence(s) can be provided on another expression cassette.

The transcriptional initiation region, the promoter, may be native or analogous or foreign or heterologous to the plant host. Additionally, the promoter
15 may be the natural sequence or alternatively a synthetic sequence. By foreign is intended that the transcriptional initiation region is not found in the native plant into which the transcriptional initiation region is introduced. As used herein a chimeric gene comprises a coding sequence operably linked to a transcription initiation region that is heterologous to the coding sequence.

20 While it may be preferable to express the sequences using heterologous promoters, the native promoter sequences may be used. Such constructs would change expression levels of acetyl-CoA synthetase in the plant or plant cell. Thus, the phenotype of the plant or plant cell is altered.

The transcriptional cassette will include in the 5'-to-3' direction of
25 transcription, a transcriptional and translational initiation region, a acetyl-CoA synthetase sequence, and a transcriptional and translational termination region functional in plants. The termination region may be native with the transcriptional initiation region, may be native with the DNA sequence of interest, or may be derived from another source. Convenient termination regions are available from
30 the Ti-plasmid of *A. tumefaciens*, such as the octopine synthase and nopaline synthase termination regions. See also Guerineau *et al.* (1991) *Mol. Gen. Genet.* 262:141-144; Proudfoot (1991) *Cell* 64:671-674; Sanfacon *et al.* (1991) *Genes Dev.* 5:141-149; Mogen *et al.* (1990) *Plant Cell.* 2:1261-1272; Munroe *et al.*

(1990) *Gene* 91:151-158; Ballas *et al.* (1989) *Nucleic Acids Res.* 17:7891-7903; Joshi *et al.* (1987) *Nucleic Acids Res.* 15:9627-9639.

Where appropriate, the gene(s) may be optimized for increased expression in the transformed plant. That is, the genes can be synthesized using plant-preferred codons for improved expression. See, for example, Campbell and Gowri
5 preferred codons for improved expression. See, for example, Campbell and Gowri (1990) *Plant Physiol.* 92:1-11 for a discussion of host-preferred codon usage. Methods are available in the art for synthesizing plant-preferred genes. See, for example, U.S. Patent Nos. 5,380,831, 5,436,391, and Murray *et al.* (1989) *Nucleic Acids Res.* 17:477-498, herein incorporated by reference.

10 Additional sequence modifications are known to enhance gene expression in a cellular host. These include elimination of sequences encoding spurious polyadenylation signals, exon-intron splice site signals, transposon-like repeats, and other such well-characterized sequences that may be deleterious to gene expression. The G-C content of the sequence may be adjusted to levels average for
15 a given cellular host, as calculated by reference to known genes expressed in the host cell. When possible, the sequence is modified to avoid predicted hairpin secondary mRNA structures.

The expression cassettes may additionally contain 5' leader sequences in the expression cassette construct. Such leader sequences can act to enhance
20 translation. Translation leaders are known in the art and include: picornavirus leaders, for example, EMCV leader (Encephalomyocarditis 5' noncoding region) (Elroy-Stein *et al.* (1989) *PNAS USA* 86:6126-6130); potyvirus leaders, for example, TEV leader (Tobacco Etch Virus) (Allison *et al.* (1986); MDMV leader (Maize Dwarf Mosaic Virus); *Virology* 154:9-20), and human immunoglobulin
25 heavy-chain binding protein (BiP), (Macejak *et al.* (1991) *Nature* 353:90-94); untranslated leader from the coat protein mRNA of alfalfa mosaic virus (AMV RNA 4) (Jobling *et al.* (1987) *Nature* 325:622-625); tobacco mosaic virus leader (TMV) (Gallie *et al.* (1989) in *Molecular Biology of RNA*, ed. Cech (Liss, New York), pp. 237-256); and maize chlorotic mottle virus leader (MCMV) (Lommel *et al.* (1991) *Virology* 81:382-385). See also, Della-Cioppa *et al.* (1987) *Plant Physiol.* 84:965-968. Other methods known to enhance translation can also be
30 utilized, for example, introns, and the like.

In preparing the expression cassette, the various DNA fragments may be manipulated, so as to provide for the DNA sequences in the proper orientation and, as appropriate, in the proper reading frame. Toward this end, adapters or linkers may be employed to join the DNA fragments or other manipulations may be involved to provide for convenient restriction sites, removal of superfluous DNA, removal of restriction sites, or the like. For this purpose, *in vitro* mutagenesis, primer repair, restriction, annealing, resubstitutions, *e.g.*, transitions and transversions, may be involved.

Generally, the expression cassette will comprise a selectable marker gene for the selection of transformed cells. Selectable marker genes are utilized for the selection of transformed cells or tissues. Marker genes include genes encoding antibiotic resistance, such as those encoding neomycin phosphotransferase II (NEO) and hygromycin phosphotransferase (HPT), as well as genes conferring resistance to herbicidal compounds, such as glufosinate ammonium, bromoxynil, imidazolinones, and 2,4-dichlorophenoxyacetate (2,4-D). See generally, Yarranton (1992) *Curr. Opin. Biotech.* 3:506-511; Christopherson *et al.* (1992) *Proc. Natl. Acad. Sci. USA* 89:6314-6318; Yao *et al.* (1992) *Cell* 71:63-72; Reznikoff (1992) *Mol. Microbiol.* 6:2419-2422; Barkley *et al.* (1980) in *The Operon*, pp. 177-220; Hu *et al.* (1987) *Cell* 48:555-566; Brown *et al.* (1987) *Cell* 49:603-612; Figge *et al.* (1988) *Cell* 52:713-722; Deuschle *et al.* (1989) *Proc. Natl. Acad. Sci. USA* 86:5400-5404; Fuerst *et al.* (1989) *Proc. Natl. Acad. Sci. USA* 86:2549-2553; Deuschle *et al.* (1990) *Science* 248:480-483; Gossen (1993) Ph.D. Thesis, University of Heidelberg; Reines *et al.* (1993) *Proc. Natl. Acad. Sci. USA* 90:1917-1921; Labow *et al.* (1990) *Mol. Cell. Biol.* 10:3343-3356; Zambretti *et al.* (1992) *Proc. Natl. Acad. Sci. USA* 89:3952-3956; Baim *et al.* (1991) *Proc. Natl. Acad. Sci. USA* 88:5072-5076; Wyborski *et al.* (1991) *Nucleic Acids Res.* 19:4647-4653; Hillenand-Wissman (1989) *Topics Mol. Struc. Biol.* 10:143-162; Degenkolb *et al.* (1991) *Antimicrob. Agents Chemother.* 35:1591-1595; Kleinschmidt *et al.* (1988) *Biochemistry* 27:1094-1104; Bonin (1993) Ph.D. Thesis, University of Heidelberg; Gossen *et al.* (1992) *Proc. Natl. Acad. Sci. USA* 89:5547-5551; Oliva *et al.* (1992) *Antimicrob. Agents Chemother.* 36:913-919; Hlavka *et al.* (1985) *Handbook of Experimental Pharmacology*, Vol. 78 (Springer-Verlag, Berlin); Gill *et al.* (1988) *Nature* 334:721-724. Such disclosures are herein incorporated by reference.

The above list of selectable marker genes is not meant to be limiting. Any selectable marker gene can be used in the present invention.

Specific embodiments of the present invention will require that antisense constructions of nucleotide sequences of interest be constructed. The antisense constructs will contain at least a portion of the messenger RNA (mRNA) for the nucleotide sequences. Antisense nucleotides are constructed to hybridize with the corresponding mRNA. Modifications of the antisense sequences may be made as long as the sequences hybridize to and interfere with expression of the corresponding mRNA. In this manner, antisense constructions having 70%, preferably 80%, more preferably 85% sequence similarity to the corresponding antisense sequences may be used. Furthermore, portions of the antisense nucleotides may be used to disrupt the expression of the target gene. Generally, sequences of at least 50 nucleotides, 100 nucleotides, 200 nucleotides, or greater may be used.

The sequences of the present invention can be used to transform or transfect any plant. In this manner, genetically modified plants, plant cells, plant tissue, seed, and the like can be obtained. Transformation protocols as well as protocols for introducing nucleotide sequences into plants may vary depending on the type of plant or plant cell, i.e., monocot or dicot, targeted for transformation. Suitable methods of introducing nucleotide sequences into plant cells and subsequent insertion into the plant genome include microinjection (Crossway *et al.* (1986) *Biotechniques* 4:320-334), electroporation (Riggs *et al.* (1986) *Proc. Natl. Acad. Sci. USA* 83:5602-5606, *Agrobacterium*-mediated transformation (Townsend *et al.*, U.S. Pat No. 5,563,055), direct gene transfer (Paszkowski *et al.* (1984) *EMBO J.* 3:2717-2722), and ballistic particle acceleration (see, for example, Sanford *et al.*, U.S. Patent No. 4,945,050; Tomes *et al.* (1995) "Direct DNA Transfer into Intact Plant Cells via Microprojectile Bombardment," in *Plant Cell, Tissue, and Organ Culture: Fundamental Methods*, ed. Gamborg and Phillips (Springer-Verlag, Berlin); and McCabe *et al.* (1988) *Biotechnology* 6:923-926). Also see Weissinger *et al.* (1988) *Ann. Rev. Genet.* 22:421-477; Sanford *et al.* (1987) *Particulate Science and Technology* 5:27-37 (onion); Christou *et al.* (1988) *Plant Physiol.* 87:671-674 (soybean); McCabe *et al.* (1988) *Bio/Technology* 6:923-926 (soybean); Finer and McMullen (1991) *In Vitro Cell Dev. Biol.*

- 27P:175-182 (soybean); Singh *et al.* (1998) *Theor. Appl. Genet.* 96:319-324 (soybean); Datta *et al.* (1990) *Biotechnology* 8:736-740 (rice); Klein *et al.* (1988) *Proc. Natl. Acad. Sci. USA* 85:4305-4309 (maize); Klein *et al.* (1988) *Biotechnology* 6:559-563 (maize); Tomes, U.S. Patent No. 5,240,855; Buising *et al.*, U.S. Patent Nos. 5,322,783 and 5,324,646; Tomes *et al.* (1995) "Direct DNA Transfer into Intact Plant Cells via Microprojectile Bombardment," in *Plant Cell, Tissue, and Organ Culture: Fundamental Methods*, ed. Gamborg (Springer-Verlag, Berlin) (maize); Klein *et al.* (1988) *Plant Physiol.* 91:440-444 (maize); Fromm *et al.* (1990) *Biotechnology* 8:833-839 (maize); Hooykaas-Van Slogteren *et al.* (1984) *Nature (London)* 311:763-764; Bowen *et al.*, U.S. Patent No. 5,736,369 (cereals); Bytebier *et al.* (1987) *Proc. Natl. Acad. Sci. USA* 84:5345-5349 (Liliaceae); De Wet *et al.* (1985) in *The Experimental Manipulation of Ovule Tissues*, ed. Chapman *et al.* (Longman, New York), pp. 197-209 (pollen); Kaeppler *et al.* (1990) *Plant Cell Reports* 9:415-418 and Kaeppler *et al.* (1992) *Theor. Appl. Genet.* 84:560-566 (whisker-mediated transformation); D'Halluin *et al.* (1992) *Plant Cell* 4:1495-1505 (electroporation); Li *et al.* (1993) *Plant Cell Reports* 12:250-255 and Christou and Ford (1995) *Annals of Botany* 75:407-413 (rice); Osjoda *et al.* (1996) *Nature Biotechnology* 14:745-750 (maize via *Agrobacterium tumefaciens*); all of which are herein incorporated by reference.

- The modified plant may be grown into plants in accordance with conventional ways. See, for example, McCormick *et al.* (1986) *Plant Cell. Reports* 5:81-84. These plants may then be grown, and either pollinated with the same transformed strain or different strains, and the resulting hybrid having the desired phenotypic characteristic identified. Two or more generations may be grown to ensure that the subject phenotypic characteristic is stably maintained and inherited and then seeds harvested to ensure the desired phenotype or other property has been achieved.

The following examples are offered by way of illustration and not by way of limitation.

EXPERIMENTAL

Example 1: Incorporation of Acetyl-CoA synthetase DNA sequences into Expression Vectors

The full-length acetyl-CoA synthetase clone was "captured" from a maize leaf library. The T3 priming site present in every clone was used to serve as an anchor primer for PCR reactions. Gene specific primers were designed and primary and secondary PCR reactions were performed. These reactions resulted in a ladder of products of increasing molecular weight that upon characterization represented various states of clone truncation. The product that exhibited the greatest molecular weight resulted in the addition of 450 bp of sequence to the information in the sequence database. This information was used to compile a full-length clone. Additional sequence analysis and database comparisons will be conducted.

The 5' end of HGS clone CBIFK38 was obtained via library RACE. This information was used with the partial sequence data from above to compile a putative full-length contig. Additional sequence analysis and database comparisons were conducted to determine a putative protein translation initiation site. There were several ATGs present in the sequence that could serve as initiation codons for protein translation with no clear consensus as to the correct one. Additional characterization of the clones obtained from the PCR product exhibiting the greatest molecular weight revealed that in addition to cloning the 5' end of CBIFK38, the 5' end of another Acetyl-CoA synthetase gene (CDPFM42) was also cloned in a single PCR reaction. This information provided a direct comparison to clone CBIFK38 and allowed for a determination of the start of protein translation. The two clones appear to share a very high degree of identity based on 5' protein sequence. These data were used to design 5' and 3' primers specific for each gene. PCR was used to generate products of the expected molecular weight using a maize leaf cDNA library as background. These clones should represent the complete open reading frames of CBIFK38 and CDPFM42. These products were cloned into the TA cloning vector pCRII-TOPO.

Primer pairs were designed for the clones representing the complete open reading frames of CBIFK38 and CDPFM42 to allow both stands to be completely sequenced.

Multiple sequencing runs have been assembled into full length contigs for HGS clones CBIFK38 and CDPFM42. The contigs have also been completely edited to give two final consensus sequences. These data were analyzed to decide

upon a cloning strategy for insertion of the open reading frames into a pET expression vector. Appropriate primers have been designed for inserting both genes as *Nco* I/*Xho* I fragments into pET 15b. Vector construction of two ACoAS::pET 15b expression constructs has been completed for HGS clones
5 CBIFK38 and CDPFM42. Clones have been transformed into the expression host BL21(DE3)pLysS. Induction and expression studies are pending.

Example 2: Transformation and Regeneration of Maize Callus

Immature maize embryos from greenhouse donor plants are bombarded
10 with a plasmid containing acetyl-CoA synthetase operably linked to a Ubiquitin promoter and containing the PinII terminator sequences (Figure 1). In addition, this plasmid also contains the selectable marker gene PAT (Wohlleben *et al.* (1988) *Gene* 70:25-37) that confers resistance to the herbicide Bialaphos. Transformation is performed as follows. All media recipes are in the Appendix.

15

Preparation of Target Tissue

The ears are surface sterilized in 30% Chlorox bleach plus 0.5% Micro detergent for 20 minutes, and rinsed two times with sterile water. The immature embryos are excised and placed embryo axis side down (scutellum side up), 25
20 embryos per plate, on 560Y medium for 4 hours and then aligned within the 2.5-cm target zone in preparation for bombardment.

Preparation of DNA

A plasmid vector comprising the acetyl-CoA synthetase operably linked to
25 a Ubiquitin promoter and containing the PinII terminator sequences is generated. This plasmid also contains the selectable marker gene PAT. The plasmid is precipitated onto 1.1 μ m (average diameter) tungsten pellets using a CaCl_2 precipitation procedure as follows:

- 100 μ l prepared tungsten particles in water
- 30 10 μ l (1 μ g) DNA in TrisEDTA buffer (1 μ g total)
- 100 μ l 2.5 M CaCl_2
- 10 μ l 0.1 M spermidine

Each reagent is added sequentially to the tungsten particle suspension, while maintained on the multitube vortexer. The final mixture is sonicated briefly and allowed to incubate under constant vortexing for 10 minutes. After the precipitation period, the tubes are centrifuged briefly, liquid removed, washed with 500 ml 100% ethanol, and centrifuged for 30 seconds. Again the liquid is removed, and 105 μ l 100% ethanol is added to the final tungsten particle pellet. For particle gun bombardment, the tungsten/DNA particles are briefly sonicated and 10 μ l spotted onto the center of each macrocarrier and allowed to dry about 2 minutes before bombardment.

10

Particle Gun Treatment

The sample plates are bombarded at level #4 in particle gun #HE34-1 or #HE34-2. All samples receive a single shot at 650 PSI, with a total of ten aliquots taken from each tube of prepared particles/DNA.

15

Subsequent Treatment

Following bombardment, the embryos are kept on 560Y medium for 2 days, then transferred to 560R selection medium containing 3 mg/liter Bialaphos, and subcultured every 2 weeks. After approximately 10 weeks of selection, selection-resistant callus clones are transferred to 288J medium to initiate plant regeneration. Following somatic embryo maturation (2-4 weeks), well-developed somatic embryos are transferred to medium for germination and transferred to the lighted culture room. Approximately 7-10 days later, developing plantlets are transferred to 272V hormone-free medium in tubes for 7-10 days until plantlets are well established. Plants are then transferred to inserts in flats (equivalent to 2.5" pot) containing potting soil and grown for 1 week in a growth chamber, subsequently grown an additional 1-2 weeks in the greenhouse, then transferred to classic 600 pots (1.6 gallon) and grown to maturity. Plants are monitored and scored for expression of the acetyl-CoA synthetase gene of interest.

APPENDIX**272 V**

Ingredient	Amount	Unit
D-I H ₂ O	950.000	MI
MS Salts (GIBCO 11117-074)	4.300	G
Myo-Inositol	0.100	G
MS Vitamins Stock Solution ##	5.000	MI
Sucrose	40.000	G
Bacto-Agar @	6.000	G

5

Directions:

@ = Add after bringing up to volume

Dissolve ingredients in polished D-I H₂O in sequence

Adjust to pH 5.6

10 Bring up to volume with polished D-I H₂O after adjusting pH

Sterilize and cool to 60°C.

= Dissolve 0.100 g of Nicotinic Acid; 0.020 g of Thiamine.HCL; 0.100 g of Pyridoxine.HCL; and 0.400 g of Glycine in 875.00 ml of polished D-I H₂O in sequence. Bring up to volume with polished D-I H₂O. Make in 400 ml portions.

15 Thiamine.HCL & Pyridoxine.HCL are in Dark Desiccator. Store for one month, unless contamination or precipitation occurs, then make fresh stock.

Total Volume (L) = 1.00

288 J

Ingredient	Amount	Unit
D-I H ₂ O	950.000	ml
MS Salts	4.300	g
Myo-Inositol	0.100	g
MS Vitamins Stock Solution ##	5.000	ml
Zecatin .5mg/ml	1.000	ml
Sucrose	60.000	g
Gelrite @	3.000	g
Indoleacetic Acid 0.5 mg/ml #	2.000	ml
0.1mM Absciscic Acid	1.000	ml
Bialaphos 1mg/ml #	3.000	ml

Directions:

- 5 @ = Add after bringing up to volume

Dissolve ingredients in polished D-I H₂O in sequence

Adjust to pH 5.6

Bring up to volume with polished D-I H₂O after adjusting pH

Sterilize and cool to 60°C.

- 10 Add 3.5g/L of Gelrite for cell biology.

= Dissolve 0.100 g of Nicotinic Acid; 0.020 g of Thiamine.HCL; 0.100 g of Pyridoxine.HCL; and 0.400 g of Glycine in 875.00 ml of polished D-I H₂O in sequence. Bring up to volume with polished D-I H₂O. Make in 400 ml portions.

Thiamine.HCL & Pyridoxine.HCL are in Dark Desiccator. Store for one month,

- 15 unless contamination or precipitation occurs, then make fresh stock.

Total Volume (L) = 1.00

560 R

Ingredient	Amount	Unit
D-I Water, Filtered	950.000	ml
CHU (N6) Basal Salts (SIGMA C-1416)	4.000	g
Eriksson's Vitamin Mix (1000X SIGMA-1511)	1.000	ml
Thiamine.HCL 0.4mg/ml	1.250	ml
Sucrose	30.000	g
2, 4-D 0.5mg/ml	4.000	ml
Gelrite @	3.000	g
Silver Nitrate 2mg/ml #	0.425	ml
Bialaphos 1mg/ml #	3.000	ml

Directions:

5 @ = Add after bringing up to volume

= Add after sterilizing and cooling to temp.

Dissolve ingredients in D-I H₂O in sequence

Adjust to pH 5.8 with KOH

Bring up to volume with D-I H₂O

10 Sterilize and cool to room temp.

Total Volume (L) = 1.00

560 Y

Ingredient	Amount	Unit
D-I Water, Filtered	950.000	ml
CHU (N6) Basal Salts (SIGMA C-1416)	4.000	g
Eriksson's Vitamin Mix (1000X SIGMA-1511	1.000	ml
Thiamine.HCL 0.4mg/ml	1.250	ml
Sucrose	120.000	g
2,4-D 0.5mg/ml	2.000	ml
L-Proline	2.880	g
Gelrite @	2.000	g
Silver Nitrate 2mg/ml #	4.250	ml

Directions:

5 @ = Add after bringing up to volume

= Add after sterilizing and cooling to temp.

Dissolve ingredients in D-I H₂O in sequence

Adjust to pH 5.8 with KOH

Bring up to volume with D-I H₂O

10 Sterilize and cool to room temp.

** Autoclave less time because of increased sucrose**

Total Volume (L) = 1.00

All publications and patent applications mentioned in the specification are indicative of the level of those skilled in the art to which this invention pertains.

5 All publications and patent applications are herein incorporated by reference to the same extent as if each individual publication or patent application was specifically and individually indicated to be incorporated by reference.

10 Although the foregoing invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, it will be obvious that certain changes and modifications may be practiced within the scope of the appended claims.

THAT WHICH IS CLAIMED:

1. A method for increasing the biosynthesis of a metabolite of interest in a plant seed, said method comprising transforming a plant with an expression
5 cassette comprising a seed-preferred promoter, operably linked to a nucleotide sequence encoding an acetyl-CoA synthetase, wherein said metabolite is selected from the group consisting of fatty acids, carotenoids, and amino acids, and said nucleotide sequence is selected from the group consisting of:
- a) a nucleotide sequence encoding a plant acetyl-CoA synthetase;
 - 10 b) a nucleotide sequence encoding a maize acetyl-CoA synthetase;
 - c) a nucleotide sequence comprising a sequence set forth in one of the SEQ ID NOS: 1 or 3;
 - d) a nucleotide sequence encoding a polypeptide comprising an amino acid sequence set forth in one of the SEQ ID NOS: 2 or 4;
 - 15 e) a nucleotide sequence which hybridizes under stringent conditions to the nucleotide sequences of a), b), c), or d).
2. The method of claim 1, wherein said plant seed is from an oil seed
20 plant.
3. The method of claim 2, wherein said oil seed plant is selected from the group consisting of canola, maize, *Brassica*, cotton, soybean, safflower, sunflower, palm, and coconut.
- 25 4. The method of claim 1, wherein said expression cassette further comprises a nucleotide sequence encoding a chloroplast targeting sequence operably linked to the nucleotide sequence encoding a plant acetyl-CoA synthetase.
- 30 5. The method of claim 1, wherein said promoter is a globulin 1 promoter.

6. The method of claim 1, wherein said promoter is selected from napin, EA9, or acyl carrier protein.

7. The method of claim 1, wherein said metabolite is a fatty acid.

5

8. The method of claim 7, wherein said plant is further transformed with an expression cassette comprising a promoter operably linked to a nucleotide sequence encoding a plant acetyl-CoA carboxylase.

10 9. The method of claim 1, wherein said metabolite is a carotenoid.

10. The method of claim 9, wherein said plant is further transformed with an expression cassette comprising a promoter operably linked to an anti-sense nucleotide sequence of a plant acetyl-CoA carboxylase.

15

11. A method for increasing fatty acid biosynthesis in a plant embryo, said method comprising transforming a plant with an expression cassette comprising a seed preferred promoter, operably linked to a nucleotide sequence, wherein said nucleotide sequence is selected from the group consisting of:

- 20 a) a nucleotide sequence encoding a plant acetyl-CoA synthetase;
b) a nucleotide sequence encoding a maize acetyl-CoA synthetase;
c) a nucleotide sequence comprising a sequence set forth in one of the SEQ ID NOS: 1 or 3;
d) a nucleotide sequence encoding a polypeptide comprising an amino
25 acid sequence set forth in one of the SEQ ID NOS: 2 or 4;
e) a nucleotide sequence which hybridizes under stringent conditions to the nucleotide sequences of a), b), c), or d).

12. The method of claim 11, wherein said expression cassette further
30 comprises a nucleotide sequence encoding a chloroplast targeting sequence operably linked to the nucleotide sequence encoding a plant acetyl-CoA synthetase.

13. The method of claim 11, wherein said promoter is a globulin 1 promoter.

14. A method for increasing the oil content of a plant seed, said method
5 comprising transforming a plant with an expression cassette comprising a seed-preferred promoter, operably linked to a nucleotide sequence said nucleotide sequence selected from the group consisting of:

- a) a nucleotide sequence encoding a plant acetyl-CoA synthetase;
- 10 b) a nucleotide sequence encoding a maize acetyl-CoA synthetase;
- c) a nucleotide sequence comprising a sequence set forth in one of the SEQ ID NOS: 1 or 3;
- d) a nucleotide sequence encoding a polypeptide comprising an
15 amino acid sequence set forth in one of the SEQ ID NOS: 2 or 4;
- e) a nucleotide sequence which hybridizes under stringent conditions to the nucleotide sequences of a), b), c), or d).

15. The method of claim 14, wherein said expression cassette further
20 comprises a nucleotide sequence encoding a chloroplast targeting sequence operably linked to the nucleotide sequence encoding a plant acetyl-CoA synthetase.

16. The method of claim 14, wherein said promoter is selected from
25 napin, EA9, or acyl carrier protein.

17. The method of claim 14, wherein said promoter is a globulin 1 promoter.

30 18. The method of claim 14, wherein said plant is further transformed with an expression cassette comprising a promoter operably linked to a nucleotide sequence encoding a plant acetyl-CoA carboxylase.

19. The method of claim 14, wherein said plant seed is from an oil seed plant.

20. The method of claim 19, wherein said oil seed plant is selected from the group consisting of canola, maize, *Brassica*, cotton, soybean, safflower, sunflower, palm, and coconut.

21. A method for increasing carotenoid levels in a plant seed, said method comprising transforming a plant with an expression cassette comprising a seed-preferred promoter, operably linked to a nucleotide sequence wherein said nucleotide sequence is selected from the group consisting of:

- a) a nucleotide sequence encoding a plant acetyl-CoA synthetase;
- b) a nucleotide sequence encoding a maize acetyl-CoA synthetase;
- c) a nucleotide sequence comprising a sequence set forth in one of the SEQ ID NOS: 1 or 3;
- d) a nucleotide sequence encoding a polypeptide comprising an amino acid sequence set forth in one of the SEQ ID NOS: 2 or 4;
- e) a nucleotide sequence which hybridizes under stringent conditions to the nucleotide sequences of a), b), c), or d).

22. The method of claim 21, wherein said expression cassette further comprises a nucleotide sequence encoding a chloroplast targeting sequence operably linked to the nucleotide sequence encoding a plant acetyl-CoA synthetase.

23. The method of claim 21, wherein said promoter is a globulin-1 promoter.

24. The method of claim 21, wherein said plant is further transformed with an expression cassette comprising a promoter operably linked to an anti-sense nucleotide sequence of a plant acetyl-CoA carboxylase.

25. An isolated nucleotide sequence, said nucleotide sequence is selected from the group consisting of:

- a) a nucleotide sequence encoding a plant acetyl-CoA synthetase;
- b) a nucleotide sequence encoding a maize acetyl-CoA synthetase;
- 5 c) a nucleotide sequence comprising a sequence set forth in one of the SEQ ID NOS: 1 or 3;
- d) a nucleotide sequence encoding a polypeptide comprising an amino acid sequence set forth in one of the SEQ ID NOS: 2 or 4;
- e) a nucleotide sequence which hybridizes under stringent
- 10 conditions to the nucleotide sequences of a), b), c), or d).

26. The nucleotide sequence of claim 25, wherein said sequence is operably linked to a seed-preferred promoter.

15 27. The nucleotide sequence of claim 26, wherein said acetyl-CoA synthetase sequence is operably linked to a nucleotide sequence encoding a chloroplast transit peptide.

28. An isolated polypeptide selected from the group consisting of:

- 20 a) a polypeptide comprising an amino acid sequence set forth in one of the SEQ ID NOS: 2 or 4;
- b) a polypeptide encoded by a nucleotide sequence comprising the sequence set forth in one of the SEQ ID NOS: 1 or 3;
- c) a polypeptide encoded by a nucleotide sequence that
- 25 hybridizes under stringent conditions to a nucleotide sequence set forth in one of the SEQ ID NOS: 1 or 3.

29. A transformed plant, said plant having stably incorporated into its genome an expression cassette, said expression cassette comprising a plant

30 promoter operably linked to a nucleotide sequence said sequence is selected from the group consisting of:

- a) a nucleotide sequence encoding a plant acetyl-CoA synthetase;

- b) a nucleotide sequence encoding a maize acetyl-CoA synthetase;
- c) a nucleotide sequence comprising a sequence set forth in one of the SEQ ID NOS: 1 or 3;
- 5 d) a nucleotide sequence encoding a polypeptide comprising an amino acid sequence set forth in one of the SEQ ID NOS: 2 or 4;
- e) a nucleotide sequence which hybridizes under stringent conditions to the nucleotide sequences of a), b), c), or d).
- 10 30. The plant of claim 29, wherein said expression cassette further comprises a nucleotide sequence encoding a chloroplast targeting sequence operably linked to the nucleotide sequence encoding acetyl-CoA synthetase.
- 15 31. The plant of claim 29, wherein said promoter is selected from seed-specific and embryo-specific promoters.
32. The plant of claim 29, wherein said plant is an oil seed plant.
- 20 33. The plant of claim 32, wherein said plant is selected from the group consisting of canola, maize, *Brassica*, cotton, soybean, safflower, sunflower, palm, and coconut.
34. The plant of claim 29, wherein said plant is maize.
- 25 35. The plant of claim 29, wherein said plant is further transformed with an expression cassette comprising a promoter operably linked to a nucleotide sequence of a plant acetyl-CoA carboxylase.
- 30 36. The transformed plant of claim 29, wherein said plant is further transformed with an expression cassette comprising a promoter operably linked to an anti-sense nucleotide sequence of a plant acetyl-CoA carboxylase.
37. Seed of the plant of any one of claims 29-36.

38. The seed of claim 37, wherein said seed has an increased amount of a fatty acid.
- 5 39. The seed of claim 37, wherein said seed has an increased amount of a carotenoid.
40. The seed of claim 37, wherein said seed has an increased amount of amino acids.
- 10 41. A transformed plant cell, said plant cell having stably incorporated into its genome an expression cassette, said expression cassette comprising a plant cell promoter operably linked to a nucleotide sequence, wherein said sequence is selected from the group consisting of:
- 15 a) a nucleotide sequence encoding a plant acetyl-CoA synthetase;
b) a nucleotide sequence encoding a maize acetyl-CoA synthetase;
c) a nucleotide sequence comprising a sequence set forth in one of the SEQ ID NOS: 1 or 3;
20 d) a nucleotide sequence encoding a polypeptide comprising an amino acid sequence set forth in one of the SEQ ID NOS: 2 or 4;
e) a nucleotide sequence which hybridizes under stringent conditions to the nucleotide sequences of a), b), c), or d).
- 25 42. The plant cell of claim 41, wherein said expression cassette further comprises a nucleotide sequence encoding a chloroplast targeting sequence operably linked to the nucleotide sequence encoding acetyl-CoA synthetase.
- 30 43. The plant cell of claim 41, wherein said promoter is a seed-preferred promoter.
44. The plant cell of claim 41, wherein said plant cell is from an oil seed plant.

45. The plant cell of claim 44, wherein said oil seed plant is selected from the group consisting of canola, maize, *Brassica*, cotton, soybean, safflower, sunflower, palm, and coconut.

5

46. The plant cell of claim 41, wherein said plant is maize.

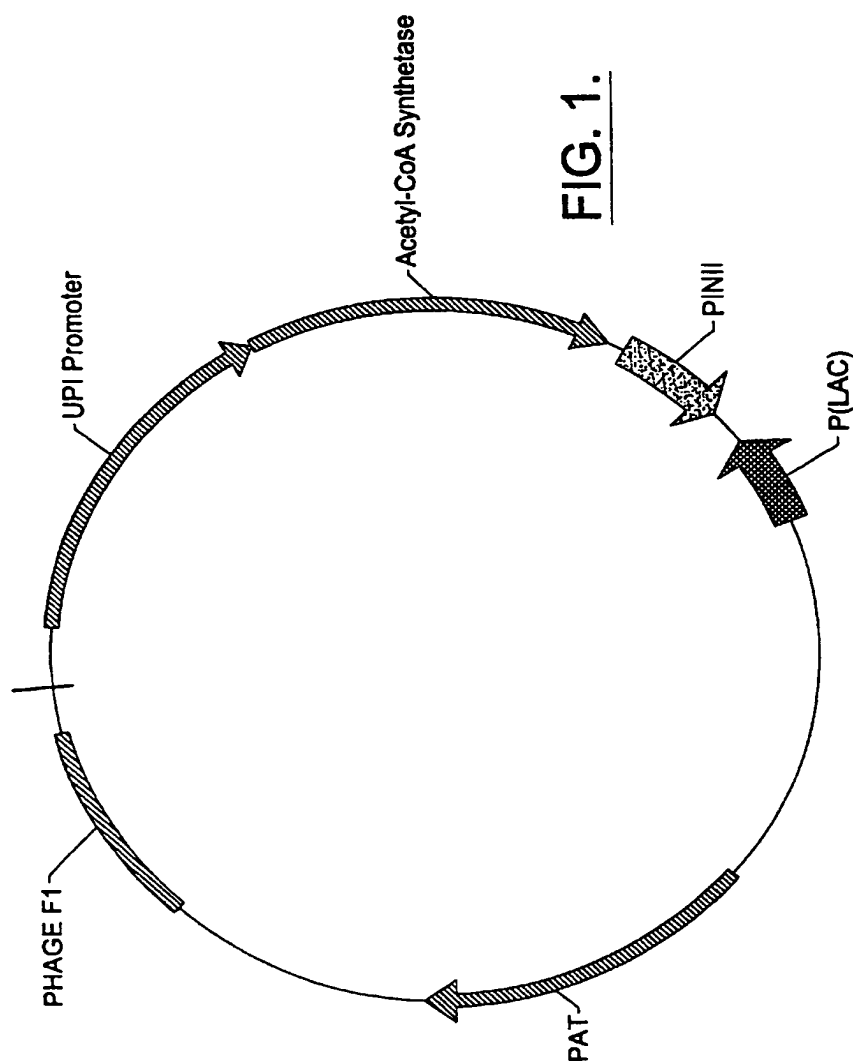


FIG. 1.

SUBSTITUTE SHEET (RULE 26)

SEQUENCE LISTING

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Bowen, Benjamin A.
Zun, Wang

<120> Compositions and Methods for Altering an
Acetyl-CoA Metabolic Pathway of a Plant

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Phe Trp Ser Glu Ile Ala Glu Thr Phe Tyr Trp Lys Glu Lys Trp Asn
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Asp	Cys	Lys	Pro	Lys	Leu	Val	Ile	Thr	Cys	Asn	Ala	Val	Lys	Arg	Gly	
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gtc	aag	ccc	atc	ttt	ctc	aaa	gat	ata	gtg	gat	gca	gct	ttg	gtt	gaa	639
Val	Lys	Pro	Ile	Phe	Leu	Lys	Asp	Ile	Val	Asp	Ala	Ala	Leu	Val	Glu	
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Ser	Glu	Lys	Asn	Gly	Val	Ser	Val	Gly	Leu	Cys	Leu	Thr	Tyr	Glu	Asn	
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INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 99/18011

A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C12N15/82 C12N15/52 C11B1/00 C07C403/24 C12N5/10
A01H5/00

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12N C11B C07C A01H

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	BEHAL, R.H., ET AL.: "Arabidopsis thaliana acetyl-CoA synthetase mRNA, complete cds" EMBL ACCESSION NO:AF036618, 5 January 1998 (1998-01-05), XP002126950	25,28
Y	the whole document	1-7,9, 11-17, 19-23, 26,27, 29-34, 37-46

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☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

Special categories of cited documents

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

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International Application No.

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